Amendments to the Specification:

Please amend the specification as follows:

Please replace the paragraph starting at page 11, line 16, with the following rewritten paragraph:

~~Figure 4.~~ Figures 4A and 4B. Serum Profiling of SAX Chip Prepared by Blending.

Please replace the paragraph starting at page 12, line 5, with the following rewritten paragraph:

~~Figure 10.~~ Figures 10A and 10B. Serum Profiling of DEAE Dextran Chip Prepared by Blending.

Please replace the paragraph starting at page 12, line 6, with the following rewritten paragraph:

~~Figure 11.~~ Figures 11A and 11B. MEP Dyed with Ponceau S.

Please replace the paragraph starting at page 12, line 7, with the following rewritten paragraph:

~~Figure 12.~~ Figures 12A, 12B and 12C. Selective binding/washing of IgG on MEP

Please replace the paragraph starting at page 12, line 8, with the following rewritten paragraph:

~~Figure 13.~~ Figures 13A, 13B and 13C. Profiling of Albumin Depleted Serum

Please replace the paragraph starting at page 12, line 9, with the following rewritten paragraph:

~~Figure 14.~~ Figures 14A, 14B and 14C. Profiling of Albumin Depleted Serum

Please replace the paragraph starting at page 12, line 10, with the following rewritten paragraph:

~~Figure 15.~~ Figures 15A, 15B and 15C. Profiling of Albumin Depleted Serum

Please replace the paragraph bridging pages 54 and 55, with the following rewritten paragraph:

In the context of SELDI analysis, moreover, the SAX chips prepared with blending method and with copolymerization method have essentially identical features. Both strongly bound milk protein sample in 50 mM pH 9.0 Tris-HCl buffer solution. For protocols of using ProteinChip, see, for example, WO 00/66265 (Rich et al., "Probes for a Gas Phase Ion Spectrometer," November 9, 2000). ~~Figure 4 shows~~ Figures 4A and 4B show the composite mass spectrum of the SAX chips prepared with blending method at low and high molecular mass of protein recognition profile. The profile shows the proteins retained on the SAX probe.

Please replace the paragraph starting at page 60, line 8, with the following rewritten paragraph:

In the context of SELDI analysis, moreover, the DEAE dextran chips strongly bound albumin depleted human serum in 50 mM pH 7.5 Tris-HCl buffer solution. For protocols of using ProteinChip, see, for example, WO 00/66265 (Rich et al., "Probes for a Gas Phase Ion Spectrometer," November 9, 2000). ~~Figure 10 shows~~ Figures 10A and 10B show the composite mass spectrum at low and high molecular mass of albumin depleted human serum protein recognition profile. The profile shows the serum proteins retained on the DEAE dextran probe.